

175409 me

STIC-Biotech/ChemLib

From: Akhavan, Ramin  
Sent: Friday, December 30, 2005 12:19 PM  
To: STIC-Biotech/ChemLib  
Subject: 10/688,299

Contacts: STIC-Biotech/ChemLib

Please conduct a standard search of the following:

1. SID 19

2. SID 51

2C70

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(STIC)

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 6, 2006, 14:34:06 ; Search time 134 Seconds

(without alignments)  
65.579 Million cell updates/sec

Title: US-10-688-299-19

Perfect score: 95  
Sequence: 1 MYRMLSLGIALSLALVTNS 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003s: \*  
7: geneseqp2004s: \*  
8: geneseqp2005s: \*  
9: geneseqp2006s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	20	1 AAP60901	AAP60901 Sequence
2	95	100.0	20	2 AAR27274	AAR27274 IL2 Signa
3	95	100.0	20	3 AAY43834	AAY43834 Secretary
4	95	100.0	20	4 AAY88092	AAY88092 IL-2 secr
5	95	100.0	20	5 AAB35082	AAB35082 IL-2 secr
6	95	100.0	20	6 AAB45952	AAB45952 Transdomi
7	95	100.0	20	7 ABB399149	ABB399149 IL-2 secr
8	95	100.0	20	8 AAV76401	AAV76401 Interleuk
9	95	100.0	20	9 AAE28695	AAE28695 Interleuk
10	95	100.0	20	10 AAB32975	AAB32975 Interleuk
11	95	100.0	20	11 AAG38473	AAG38473 Signal pe
12	95	100.0	20	12 ABU64910	ABU64910 Interleuk
13	95	100.0	20	13 ABU64805	ABU64805 Interleuk
14	95	100.0	20	14 ABP56570	ABP56570 IL-2 secr
15	95	100.0	20	15 ABR39532	ABR39532 IL-2 sign
16	95	100.0	20	16 AAB33898	AAB33898 Human int
17	95	100.0	20	17 ABU14038	ABU14038 Interleuk
18	95	100.0	20	18 ABP72891	ABP72891 Interleuk
19	95	100.0	20	19 ABU09663	ABU09663 Interleuk
20	95	100.0	20	20 ABA07066	ABA07066 Interleuk
21	95	100.0	20	21 ADA07015	ADA07015 IL-2 secr
22	95	100.0	20	22 ADB66862	ADB66862 Fusion nu
23	95	100.0	20	23 AAE39843	AAE39843 Interleuk
24	95	100.0	20	24 ADD28919	ADD28919 Interleuk

25	95	100.0	20	7 ADE10754	ADE10754 Structura
26	95	100.0	20	7 ADF90387	ADF90387 Secretary
27	95	100.0	20	7 ABU64387	ABU64387 Interleuk
28	95	100.0	20	7 ADI26400	ADI26400 Interleuk
29	95	100.0	20	7 ADJ53830	ADJ53830 Interleuk
30	95	100.0	20	8 ADI36233	ADI36233 Interleuk
31	95	100.0	20	8 ADK15773	ADK15773 Fusion pr
32	95	100.0	20	8 ADM24765	ADM24765 Interleuk
33	95	100.0	20	8 ADI23804	ADI23804 Interleuk
34	95	100.0	20	9 ADK55475	ADK55475 IL-2 secr
35	95	100.0	20	9 ADY21050	ADY21050 Transdomi
36	95	100.0	20	9 ADZ64559	ADZ64559 Human IL-
37	95	100.0	20	9 ABB53570	ABB53570 IL-2 secr
38	95	100.0	23	6 ADA14765	ADA14765 Human int
39	95	100.0	23	6 ABB73285	ABB73285 Renilla r
40	95	100.0	23	6 ADA37434	ADA37434 Human int
41	95	100.0	23	8 ADA33967	ADA33967 Human int
42	95	100.0	23	9 ABB25493	ABB25493 Interleuk
43	95	100.0	26	6 ABU10201	ABU10201 Interleuk
44	95	100.0	49	2 AAR83059	AAR83059 Human IL-
45	95	100.0	64	6 ABP70796	ABP70796 Human ext

#### ALIGNMENTS

RESULT 1  
ID AAP60901 standard; peptide; 20 AA.  
AC AAP60901;  
XX  
XX  
DT 25-MAR-2003 (revised)  
DT 03-JUL-1991 (first entry)  
XX  
XX  
DE Sequence N-terminal to novel human T-cell growth factor.  
XX  
XX atCCF; antitumour; cancer; IL-2; immunoregulatory; AIDS; cytomegalovirus;  
XX herpes; tuberculosis; leprosis.  
XX  
XX Homo sapiens.  
XX  
XX W08505124-A.  
XX  
XX 21-NOV-1985.  
XX  
XX 02-MAY-1985; 85WO-EP000194.  
XX  
XX 08-MAY-1984; 84US-00608228.  
XX 07-APR-1986; 86US-00849234.  
XX  
XX (SANO ) SANDOZ AG.  
XX (GEMT ) GENETICS INST INC.  
XX  
XX Clark SC;  
XX  
XX WPI; 1986-028179/04.  
XX  
XX New human T-cell growth factor from m-RNA of plasma source - useful as  
XX immuno-regulatory agent for therapeutic use, as antimycotic and antiviral  
XX agent, for assisting antitumour treatments etc.  
XX  
XX Claim 4; Page 54; 66pp; English.  
XX  
XX Human T-cell growth factor (atCCF) is distinct from TCGF (IL-2) may be  
XX purified and recovered with a higher yield. It is useful in supporting  
XX activated mammalian T-cell growth eg. in culture media. It may also be  
XX used as an antimycotic, immunoregulatory antiviral and antibacterial  
XX agent treating AIDS, SCIDS, congenital immuno-deficiency,  
XX cytomegalovirus and herpes infections, tuberculosis and leprosis.  
XX (Updated on 25-MAR-2003 to correct PA field.)  
XX  
XX Sequence 20 AA;

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 4, 2006, 15:22:52 : Search time 3720 Seconds

(without alignments)  
12544.671 Million cell updates/sec

Title: US-10-688-299-51

Perfect score: 7002  
Sequence: 1 tggccatgcatactgtgta.....taccgcatacagattgacctat 7002

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: N Geneseq 21:\*

1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*  
14: Geneseqn2005as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7002	100.0	7002	14	ADZ64591 Expressio
2	6029.2	86.1	7802	14	ADZ64590 Expressio
3	5797.8	82.8	7940	14	ADZ64589 Expressio
4	3088.8	44.1	10769	14	ADZ64586 Expressio
5	3055.6	43.6	8152	14	ADW01011 Exemplary
6	2955.2	42.2	7037	6	ABK91461 Modified
7	2948.8	42.1	7042	6	ABK91457 Modified
8	2935.8	41.9	6965	6	ABK91459 Modified
9	2934.8	41.9	6970	6	ABK91454 Modified
10	2928.2	41.8	7003	6	ABK91521 Modified
11	2918.8	41.7	6902	10	ACCT71562 VRC6703 (p
12	2917.2	41.7	6869	14	ADZ50977 Modified
13	2916.6	41.7	6872	6	ABK91542 Modified
14	2915.4	41.6	7003	2	AAK59390 Plasmid p
15	2913.6	41.6	6859	6	ABK91458 Modified
16	2913	41.6	7001	2	AAK89795 DNA of pV
17	2910.2	41.6	6861	6	ABK91534 Modified
18	2909.2	41.5	6978	6	AAK38657 CMVkan/R-
19	2909.2	41.5	6978	10	ABZ58706 DNA seque

20	2908.6	41.5	7099	4	AAH22814 DNA seque
21	2908.4	41.5	6940	10	ACCT71535
22	2907.2	41.5	6856	6	ABK91462 Modified
23	2906.8	41.5	6868	10	ACCT71558
24	2905.8	41.5	6836	6	ABK91540 Modified
25	2904.6	41.5	7002	10	ACCT71536
26	2903.6	41.5	6846	6	ABK91537
27	2903.2	41.5	6913	10	ACCT71531
28	2902	41.4	6853	6	ABK91538
29	2901.2	41.4	7023	10	ACCT71541
30	2899	41.4	6829	6	ABK91544
31	2899	41.4	6829	14	ADZ50978
32	2898.8	41.4	6889	10	ACCT71539
33	2898.6	41.4	7005	10	ACCT71551
34	2897	41.4	7036	10	ACCT71537
35	2896.8	41.4	7073	2	AAK59391
36	2896.8	41.4	7072	2	AAK89796
37	2896.2	41.4	6836	14	ADZ50976
38	2893.2	41.3	6914	10	ACCT71529
39	2892.8	41.3	7087	10	ACCT71534
40	2892.2	41.3	6824	6	ABK91560
41	2892.2	41.3	6885	10	ACCT71538
42	2891	41.3	6887	10	ACCT71526
43	2890.2	41.3	6800	6	ABK91541
44	2888.2	41.2	7044	10	ACCT71527
45	2887.8	41.2	5742	14	ADZ64587

## ALIGNMENTS

RESULT 1  
ID ADZ64591 standard; DNA; 7002 BP.  
XX ADZ64591;  
AC ADZ64591;  
XX 30-JUN-2005 (first entry)  
DT Expression construct RO71 DNA.  
DE  
XX vector; gene transfer; DNA cassette; delivery mechanism; cytostatic;  
XX cardiovascular-Gen.; immunosuppressive; virucide; antibacterial;  
XX anti-inflammatory; antisense therapy; cancer; autoimmune disease;  
XX cardiovascular disease; viral infection; bacterial infection;  
XX inflammation; ds.  
XX Synthetic.  
XX OS  
XX WO2005035764-A1.  
XX PD  
XX 21-APR-2005.  
XX PF  
XX 14-OCT-2004; 2004WO-CA001866.  
XX PR  
XX 16-OCT-2003; 2003US-00688299.  
XX PA (UTBR-) UNIV BRITISH COLUMBIA.  
XX PI  
XX Finn J. MacLachlan I;  
XX WPI, 2005-306367/31.  
XX DR  
XX Novel expression vector having cassette having RNA polymerase promoters,  
XX nucleic acid encoding secretable RNA polymerase having secretion domain  
XX PT and nucleic acid encoding target, useful for expressing target  
XX therapeutic compounds.  
XX PS Claim 40; SEQ ID NO 51; 117pp; English.  
XX This invention describes a novel expression vector, comprising an  
XX expression cassette having two components (a) a Cytomegalovirus-derived  
XX promoter and a first RNA polymerase promoter (preferably a T7 RNA